

0020

OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/748,451

DATE: 01/16/2001

TIME: 11:52:45

Input Set : A:\UTSD546USD1.txt

Output Set: N:\CRF3\01162001\I748451.raw

3 <110> APPLICANT: WANG, XIAODONG
 4 LIU, XUESONG
 6 <120> TITLE OF INVENTION: DNA FRAGMENTATION FACTOR INVOLVED IN APOPTOSIS
 8 <130> FILE REFERENCE: UTSD:546USD1
 C--> 10 <140> CURRENT APPLICATION NUMBER: US/09/748,451
 11 <141> CURRENT FILING DATE: 2000-12-22
 13 <150> PRIOR APPLICATION NUMBER: 09/061,702
 14 <151> PRIOR FILING DATE: 1998-04-16
 16 <160> NUMBER OF SEQ ID NOS: 21
 18 <170> SOFTWARE: PatentIn Ver. 2.1
 20 <210> SEQ ID NO: 1
 21 <211> LENGTH: 2839
 22 <212> TYPE: DNA
 23 <213> ORGANISM: Homo sapiens
 25 <400> SEQUENCE: 1

ENTERED
 see p. 5

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28 ggacatctgc aatgctccag aagcccaaga gcgtgaagct gcgggccctg cgcagcccca 180
29 ggaagtccgg cgtggctggc cggagctgcc aggaggtgct gcgcaaggcg tgtctccgct 240
30 tccagctccc tgagcgcggg tcccggctgt gcctgtacga ggatggcacg gagctgacgg 300
31 aagattactt cccagtggtt cccgacaacg ccgagctggt gctgctcacc ttgggccagg 360
32 cctggcaggy ctatgtgagc gacatcaggc gcttcctcag tgcatttcac gagccacagg 420
33 tggggctcat ccaggccggc cagcagctgc tgtgtgatga gcaggcccca cagaggcaga 480
34 ggctgctggc tgacctctg cacaacgtca gccagaacat cgcggccgag acccgggctg 540
35 aggacccgcc gtggtttgaa ggcttgaggt cccgatttca gagcaagtct ggctatctga 600
36 gatacagctg tgagagccgg atccggagtt acctgaggga ggtgagctcc taccctcca 660
37 cagtgggtgc ggaggctcag gaggaattcc tgcgggtcct cggctccatg tgccagaggc 720
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43 agaacctaaa actagtgcac attgtctgcc ataagaaaac caccacaag ctcaactgtg 1080
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45 gccagtgaca cgtacacacc acgtcctggt ctttgtttga ggcctgacgt gggcatcatt 1200
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56 gccaccttgc ttgagggaca agttgtttat gtatcagctc tctgtgggt ctccctttcc 1860
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58 ttgggggtac gatgtttata ctccgtaaag aacatacaag gacattcact gctgattttt 1980
59 ttttttgttt gtttgagaca ggggtctcact ctgtcgctca ggctggagtg cagtgatgca 2040
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61 caagtagctg ggattacagg cacctaccac cagggccagc taatttttgt atgtttagta 2160
62 gtaacggggt ttcacatgt tggccaggct gttctcgaaac tctgacctc aggtgatctg 2220
63 cccgcctcgg tctcccaaag tgctgggatt acaggcatga gccactgcac ctgacctgct 2280
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66 gattcaacct gatacattta catagtgc aaactgtgtca cagtttcagg cttttatgag 2460
67 gaaagcggtt ctgtgtagaa actggaagct gttcagggca tcggcagctg aacctgctc 2520
68 cgttggtcag cgttactatc atctcggatc atatggagct catgtcagcc gtgtgggtgg 2580
69 cgggtgcaca gagacggtct ggaaggaaac acgcggtatc gaacagcagt aatcctgggg 2640
70 gatacggggg ttgggctaga ttacagaggg ctcattttct acgtcatgta ttttatgata 2700
71 cttgaatttt ttgaaatggg catttatttt ataacatggt aaaatgtact ttttaaatta 2760
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77 <211> LENGTH: 338
78 <212> TYPE: PRT
79 <213> ORGANISM: Homo sapiens
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86             20             25             30
88 Gly Cys Leu Arg Phe Gln Leu Pro Glu Arg Gly Ser Arg Leu Cys Leu
89             35             40             45
91 Tyr Glu Asp Gly Thr Glu Leu Thr Glu Asp Tyr Phe Pro Ser Val Pro
92             50             55             60
94 Asp Asn Ala Glu Leu Val Leu Leu Thr Leu Gly Gln Ala Trp Gln Gly
95   65             70             75             80
97 Tyr Val Ser Asp Ile Arg Arg Phe Leu Ser Ala Phe His Glu Pro Gln
98             85             90             95
100 Val Gly Leu Ile Gln Ala Ala Gln Gln Leu Leu Cys Asp Glu Gln Ala
101             100            105            110
103 Pro Gln Arg Gln Arg Leu Leu Ala Asp Leu Leu His Asn Val Ser Gln
104             115            120            125
106 Asn Ile Ala Ala Glu Thr Arg Ala Glu Asp Pro Pro Trp Phe Glu Gly
107             130            135            140
109 Leu Glu Ser Arg Phe Gln Ser Lys Ser Gly Tyr Leu Arg Tyr Ser Cys
110   145            150            155            160
112 Glu Ser Arg Ile Arg Ser Tyr Leu Arg Glu Val Ser Ser Tyr Pro Ser
113             165            170            175
115 Thr Val Gly Ala Glu Ala Gln Glu Glu Phe Leu Arg Val Leu Gly Ser
116             180            185            190
118 Met Cys Gln Arg Leu Arg Ser Met Gln Tyr Asn Gly Ser Tyr Phe Asp
119             195            200            205
121 Arg Gly Ala Lys Gly Gly Ser Arg Leu Cys Thr Pro Glu Gly Trp Phe
122             210            215            220

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124 Ser Cys Gln Gly Pro Phe Asp Met Asp Ser Cys Leu Ser Arg His Ser
125 225                230                235                240
127 Ile Asn Pro Tyr Ser Asn Arg Glu Ser Arg Ile Leu Phe Ser Thr Trp
128                245                250                255
130 Asn Leu Asp His Ile Ile Glu Lys Lys Arg Thr Ile Ile Pro Thr Leu
131                260                265                270
133 Val Glu Ala Ile Lys Glu Gln Asp Gly Arg Glu Val Asp Trp Glu Tyr
134                275                280                285
136 Phe Tyr Gly Leu Leu Phe Thr Ser Glu Asn Leu Lys Leu Val His Ile
137                290                295                300
139 Val Cys His Lys Lys Thr Thr His Lys Leu Asn Cys Asp Pro Ser Arg
140 305                310                315                320
142 Ile Tyr Lys Pro Gln Thr Arg Leu Lys Arg Lys Gln Pro Val Arg Lys
143                325                330                335
145 Arg Gln
149 <210> SEQ ID NO: 3
150 <211> LENGTH: 1689
151 <212> TYPE: DNA
152 <213> ORGANISM: Homo sapiens
154 <220> FEATURE:
155 <221> NAME/KEY: CDS
156 <222> LOCATION: (113)..(1105)
158 <400> SEQUENCE: 3
159 gcgtcgaccg aactacatct cccggcaggg tgcggaaggg ggtcgagtag aaggaccgcc 60
161 gctccggcct cccgcgactt ctcgaagggt ggcaggcccc acctgtgga gg`atg gag 118
162                                     Met Glu
163                                     1
165 gtg acc ggg gac gcc ggg gta cca gaa tct ggc gag atc cgg act cta 166
166 Val Thr Gly Asp Ala Gly Val Pro Glu Ser Gly Glu Ile Arg Thr Leu
167                5                10                15
169 aag ccg tgt ctg ctg cgc cgc aac tac agc cgc gaa cag cac ggc gtg 214
170 Lys Pro Cys Leu Leu Arg Arg Asn Tyr Ser Arg Glu Gln His Gly Val
171                20                25                30
173 gcc gcc tcc tgc ctc gaa gac ctg agg agc aag gcc tgt gac att ctg 262
174 Ala Ala Ser Cys Leu Glu Asp Leu Arg Ser Lys Ala Cys Asp Ile Leu
175 35                40                45                50
177 gcc att gat aag tcc ctg aca cca gtc acc ctt gtc ctg gca gag gat 310
178 Ala Ile Asp Lys Ser Leu Thr Pro Val Thr Leu Val Leu Ala Glu Asp
179                55                60                65
181 ggc acc ata gtg gat gat gac gat tac ttt ctg tgt cta cct tcc aat 358
182 Gly Thr Ile Val Asp Asp Asp Asp Tyr Phe Leu Cys Leu Pro Ser Asn
183                70                75                80
185 act aag ttt gtg gca ttg gct agt aat gag aaa tgg gca tac aac aat 406
186 Thr Lys Phe Val Ala Leu Ala Ser Asn Glu Lys Trp Ala Tyr Asn Asn
187                85                90                95
189 tca gat gga ggt aca gct tgg att tcc caa gag tcc ttt gat gta gat 454
190 Ser Asp Gly Gly Thr Ala Trp Ile Ser Gln Glu Ser Phe Asp Val Asp
191                100                105                110
193 gaa aca gac agc ggg gca ggg ttg aag tgg aag aat gtg gcc agg gag 502

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194 Glu Thr Asp Ser Gly Ala Gly Leu Lys Trp Lys Asn Val Ala Arg Glu
195 115 120 125 130
197 ctg aaa gaa gat ctg tcc agc atc atc ctc cta tca gag gag gac ctc 550
198 Leu Lys Glu Asp Leu Ser Ser Ile Ile Leu Leu Ser Glu Glu Asp Leu
199 135 140 145
201 cag atg ctt gtt gac gct ccc tgc tca gac ctg gct cag gaa cta cgt 598
202 Gln Met Leu Val Asp Ala Pro Cys Ser Asp Leu Ala Gln Glu Leu Arg
203 150 155 160
205 cag agt tgt gcc acc gtc cag cgg ctg cag cac aca ctc caa cag gtg 646
206 Gln Ser Cys Ala Thr Val Gln Arg Leu Gln His Thr Leu Gln Gln Val
207 165 170 175
209 ctt gac caa aga gag gaa gtg cgt cag tcc aag cag ctc ctg cag ctg 694
210 Leu Asp Gln Arg Glu Glu Val Arg Gln Ser Lys Gln Leu Leu Gln Leu
211 180 185 190
213 tac ctc cag gct ttg gag aaa gag ggc agc ctc ttg tca aag cag gaa 742
214 Tyr Leu Gln Ala Leu Glu Lys Glu Gly Ser Leu Leu Ser Lys Gln Glu
215 195 200 205 210
217 gag tcc aaa gct gcc ttt ggt gag gag gtg gat gca gta gac acg ggt 790
218 Glu Ser Lys Ala Ala Phe Gly Glu Glu Val Asp Ala Val Asp Thr Gly
219 215 220 225
221 atg agc aga gag acc tcc tcg gac gtt gcg ctg gcg agc cac atc ctt 838
222 Met Ser Arg Glu Thr Ser Ser Asp Val Ala Leu Ala Ser His Ile Leu
223 230 235 240
225 act gca ctg agg gag aag cag gct cca gag ctg agc tta tct agt cag 886
226 Thr Ala Leu Arg Glu Lys Gln Ala Pro Glu Leu Ser Leu Ser Ser Gln
227 245 250 255
229 gat ttg gag ttg gtt acc aag gaa gac ccc aaa gca ctg gct gtt gcc 934
230 Asp Leu Glu Leu Val Thr Lys Glu Asp Pro Lys Ala Leu Ala Val Ala
231 260 265 270
233 ttg aac tgg gac ata aag aag acg gag act gtt cag gag gcc tgt gag 982
234 Leu Asn Trp Asp Ile Lys Lys Thr Glu Thr Val Gln Glu Ala Cys Glu
235 275 280 285 290
237 cgg gag ctc gcc ctg cgc ctg cag cag acg cag agc ttg cat tct ctc 1030
238 Arg Glu Leu Ala Leu Arg Leu Gln Gln Thr Gln Ser Leu His Ser Leu
239 295 300 305
241 cgg agc atc tca gca agc aag gcc tca cca cct ggt gac ctg cag aat 1078
242 Arg Ser Ile Ser Ala Ser Lys Ala Ser Pro Pro Gly Asp Leu Gln Asn
243 310 315 320
245 cct aag cga gcc aga cag gat ccc aca tagcagcagc gggaagtgtg 1125
246 Pro Lys Arg Ala Arg Gln Asp Pro Thr
247 325 330
249 ccaaggaagc tctgtggcgt tgtgttattg gtagacaccc tcagcctcat catttgacta 1185
251 cctatgtact actctacccc ctgccttaga gcaccttcca gagaagctat tccaggtctc 1245
253 aacatacgcc gtteccacaa tttttttttt agccccacca gcttcaggac ttctgccaat 1305
255 tttgaatgat atagctgcac caacaatatc ccgcctcttc taattacata tgatgttctc 1365
257 tgttcaaaag taattggcag tgattggcca ggcgcagtgg ctacgcctg taatcccagc 1425
259 actgggaggc cgaggggggc ggatcgtgaa gtcaggagat cgagaccatc ctggctaaca 1485
261 tggtgaaacc ctgtctctac taaaaatata aaaaaaatta gccagccatg gtggcgggcg 1545
263 cctgtaatcc cagctacttg ggaggctgag gcaggagaat ggcatgaacc tgggaggcag 1605

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265 agcttgcaagt gagctgagat tgcgccactg cactccagcc tgggcaacag agcgagactc 1665
267 cgtctcaaaa aaaaaaaaaa aaaa 1689
270 <210> SEQ ID NO: 4
271 <211> LENGTH: 331
272 <212> TYPE: PRT
273 <213> ORGANISM: Homo sapiens
275 <400> SEQUENCE: 4
276 Met Glu Val Thr Gly Asp Ala Gly Val Pro Glu Ser Gly Glu Ile Arg
277 1 5 10 15
279 Thr Leu Lys Pro Cys Leu Leu Arg Arg Asn Tyr Ser Arg Glu Gln His
280 20 25 30
282 Gly Val Ala Ala Ser Cys Leu Glu Asp Leu Arg Ser Lys Ala Cys Asp
283 35 40 45
285 Ile Leu Ala Ile Asp Lys Ser Leu Thr Pro Val Thr Leu Val Leu Ala
286 50 55 60
288 Glu Asp Gly Thr Ile Val Asp Asp Asp Tyr Phe Leu Cys Leu Pro
289 65 70 75 80
291 Ser Asn Thr Lys Phe Val Ala Leu Ala Ser Asn Glu Lys Trp Ala Tyr
292 85 90 95
294 Asn Asn Ser Asp Gly Gly Thr Ala Trp Ile Ser Gln Glu Ser Phe Asp
295 100 105 110
297 Val Asp Glu Thr Asp Ser Gly Ala Gly Leu Lys Trp Lys Asn Val Ala
298 115 120 125
300 Arg Glu Leu Lys Glu Asp Leu Ser Ser Ile Ile Leu Leu Ser Glu Glu
301 130 135 140
303 Asp Leu Gln Met Leu Val Asp Ala Pro Cys Ser Asp Leu Ala Gln Glu
304 145 150 155 160
306 Leu Arg Gln Ser Cys Ala Thr Val Gln Arg Leu Gln His Thr Leu Gln
307 165 170 175
309 Gln Val Leu Asp Gln Arg Glu Glu Val Arg Gln Ser Lys Gln Leu Leu
310 180 185 190
312 Gln Leu Tyr Leu Gln Ala Leu Glu Lys Glu Gly Ser Leu Leu Ser Lys
313 195 200 205
315 Gln Glu Glu Ser Lys Ala Ala Phe Gly Glu Glu Val Asp Ala Val Asp
316 210 215 220
318 Thr Gly Met Ser Arg Glu Thr Ser Ser Asp Val Ala Leu Ala Ser His
319 225 230 235 240
321 Ile Leu Thr Ala Leu Arg Glu Lys Gln Ala Pro Glu Leu Ser Leu Ser
322 245 250 255
324 Ser Gln Asp Leu Glu Leu Val Thr Lys Glu Asp Pro Lys Ala Leu Ala
325 260 265 270
327 Val Ala Leu Asn Trp Asp Ile Lys Lys Thr Glu Thr Val Gln Glu Ala
328 275 280 285
330 Cys Glu Arg Glu Leu Ala Leu Arg Leu Gln Gln Thr Gln Ser Leu His
331 290 295 300
333 Ser Leu Arg Ser Ile Ser Ala Ser Lys Ala Ser Pro Pro Gly Asp Leu
334 305 310 315 320
336 Gln Asn Pro Lys Arg Ala Arg Gln Asp Pro Thr
337 325 330

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY

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L:10 M:270 C: Current Application Number differs, Replaced Current Application Number

L:371 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5

L:412 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7

L:445 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8